RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/910,185

DATE: 08/02/2001
TIME: 10:56:08

Input Set : A:\RTS-0258 Sequence Listing.txt
Output Set: N:\CRF3\08022001\I910185.raw

```
      6 <110> APPLICANT: C. Frank Bennett
      7          Susan M. Freier
      9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF GLIOMA-ASSOCIATED ONCOGENE-3
EXPRESSION
     11 <130> FILE REFERENCE: RTS-0258
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/910,185
C--> 13 <141> CURRENT FILING DATE: 2001-07-18
     13 <160> NUMBER OF SEQ ID NOS: 90
     16 <210> SEQ ID NO: 1
     17 <211> LENGTH: 20
     18 <212> TYPE: DNA
     19 <213> ORGANISM: Artificial Sequence
     21 <220> FEATURE:
     23 <223> OTHER INFORMATION: Antisense Oligonucleotide
     25 <400> SEQUENCE: 1                                               20
     26 tccgtcatcg ctcctcaggg
     29 <210> SEQ ID NO: 2
     30 <211> LENGTH: 20
     31 <212> TYPE: DNA
     32 <213> ORGANISM: Artificial Sequence
     34 <220> FEATURE:
     36 <223> OTHER INFORMATION: Antisense Oligonucleotide
     38 <400> SEQUENCE: 2                                               20
     39 atgcattctg cccccaagga
     42 <210> SEQ ID NO: 3
     43 <211> LENGTH: 5055
     44 <212> TYPE: DNA
     45 <213> ORGANISM: Homo sapiens
     47 <220> FEATURE:
     49 <220> FEATURE:
     50 <221> NAME/KEY: CDS
     51 <222> LOCATION: (55)...(4845)
     53 <400> SEQUENCE: 3
     54 cgatactacg tgggcatttt tggtcgaaga gagctgaagt aatgagaaga catc atg   57
     55                                                             Met
     56                                                              1
     58 gag gcc cag tcc cac agc tcc acg acc act gaa aag aaa aaa gtt gag  105
     59 Glu Ala Gln Ser His Ser Ser Thr Thr Thr Glu Lys Lys Lys Val Glu
     60               5                  10                 15
     62 aat tcc ata gtg aag tgc tcc act cga aca gat gtg agc gag aaa gcc  153
     63 Asn Ser Ile Val Lys Cys Ser Thr Arg Thr Asp Val Ser Glu Lys Ala
     64           20                 25                 30
     66 gtt gcc tcc agc acc act tct aat gag gat gaa agt cct gga cag act  201
     67 Val Ala Ser Ser Thr Thr Ser Asn Glu Asp Glu Ser Pro Gly Gln Thr
     68           35                 40                 45
     70 tat cac aga gag aga aga aac gca atc act atg cag cca cag aat gtc  249
     71 Tyr His Arg Glu Arg Arg Asn Ala Ile Thr Met Gln Pro Gln Asn Val
     72 50                 55                 60                 65
```

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```
74  cag ggg ctc agc aaa gtc agt gag gaa cct tca aca tcg agt gac gag       297
75  Gln Gly Leu Ser Lys Val Ser Glu Glu Pro Ser Thr Ser Ser Asp Glu
76                    70                    75                    80
78  agg gcc tca ttg atc aag aaa gag atc cat ggg tcc ctg cca cac gtg       345
79  Arg Ala Ser Leu Ile Lys Lys Glu Ile His Gly Ser Leu Pro His Val
80                    85                    90                    95
82  gcg gag ccc tct gtg ccg tac cgc ggg acg gtg ttt gcc atg gac ccc       393
83  Ala Glu Pro Ser Val Pro Tyr Arg Gly Thr Val Phe Ala Met Asp Pro
84               100                   105                   110
86  agg aat ggt tac atg gag ccc cac tac cac cct cct cat ctt ttc cct       441
87  Arg Asn Gly Tyr Met Glu Pro His Tyr His Pro Pro His Leu Phe Pro
88        115                   120                   125
90  gcc ttc cat cct cct gta cca att gat gcc aga cat cat gag ggc cgt       489
91  Ala Phe His Pro Pro Val Pro Ile Asp Ala Arg His His Glu Gly Arg
92  130                   135                   140                   145
94  tac cat tac gat cca tct ccg att cct cca ttg cat atg act tcc gcc       537
95  Tyr His Tyr Asp Pro Ser Pro Ile Pro Pro Leu His Met Thr Ser Ala
96                    150                   155                   160
98  tta tct agt agc cct acg tat ccg gac ctg ccc ttc att agg atc tcc       585
99  Leu Ser Ser Ser Pro Thr Tyr Pro Asp Leu Pro Phe Ile Arg Ile Ser
100                   165                   170                   175
102 cca cac cgg aac ccc gct gct gct tcc gag tct ccc ttc agc cct cca       633
103 Pro His Arg Asn Pro Ala Ala Ala Ser Glu Ser Pro Phe Ser Pro Pro
104            180                   185                   190
106 cat ccc tac att aat ccc tac atg gac tat atc cgc tcc ttg cac agc       681
107 His Pro Tyr Ile Asn Pro Tyr Met Asp Tyr Ile Arg Ser Leu His Ser
108        195                   200                   205
110 agc cca tcg ctc tcc atg atc tca gca acc cgt ggg ctg agc cct aca       729
111 Ser Pro Ser Leu Ser Met Ile Ser Ala Thr Arg Gly Leu Ser Pro Thr
112 210                   215                   220                   225
114 gat gcg ccc cat gca gga gtc agc cca gca gaa tac tat cat cag atg       777
115 Asp Ala Pro His Ala Gly Val Ser Pro Ala Glu Tyr Tyr His Gln Met
116                   230                   235                   240
118 gcc ctg cta act ggc cag cgc agc ccc tat gca gac att att ccc tca       825
119 Ala Leu Leu Thr Gly Gln Arg Ser Pro Tyr Ala Asp Ile Ile Pro Ser
120                   245                   250                   255
122 gct gcc acc gcc ggc acg ggg gcc atc cac atg gaa tat ctt cat gct       873
123 Ala Ala Thr Ala Gly Thr Gly Ala Ile His Met Glu Tyr Leu His Ala
124            260                   265                   270
126 atg gat agc acc aga ttc tcc agc ccc agg ctg tca gcc agg ccg agc       921
127 Met Asp Ser Thr Arg Phe Ser Ser Pro Arg Leu Ser Ala Arg Pro Ser
128        275                   280                   285
130 cga aaa cgt aca ctg tcc ata tca cca ctc tcc gat cat agc ttt gac       969
131 Arg Lys Arg Thr Leu Ser Ile Ser Pro Leu Ser Asp His Ser Phe Asp
132 290                   295                   300                   305
134 ctt cag acc atg ata agg acg tct ccc aac tcc ttg gtc acg att ctc      1017
135 Leu Gln Thr Met Ile Arg Thr Ser Pro Asn Ser Leu Val Thr Ile Leu
136                   310                   315                   320
138 aat aat tcc cgt agc agc tct tca gca agt ggc tcc tat ggt cac tta      1065
```

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```
139 Asn Asn Ser Arg Ser Ser Ser Ser Ala Ser Gly Ser Tyr Gly His Leu
140             325             330             335
142 tct gca agt gca atc agc cct gcc ttg agc ttc acc tac tct tcc gcg   1113
143 Ser Ala Ser Ala Ile Ser Pro Ala Leu Ser Phe Thr Tyr Ser Ser Ala
144             340             345             350
146 ccc gtc tct ctc cac atg cat cag cag atc cta agc cga caa cag agc   1161
147 Pro Val Ser Leu His Met His Gln Gln Ile Leu Ser Arg Gln Gln Ser
148     355             360             365
150 tta ggt tca gcc ttt gga cac agc cct cca ctc atc cac cct gcc cca   1209
151 Leu Gly Ser Ala Phe Gly His Ser Pro Pro Leu Ile His Pro Ala Pro
152 370             375             380             385
154 act ttt cca aca cag agg cct att cca ggg atc cct acg gtt ctg aac   1257
155 Thr Phe Pro Thr Gln Arg Pro Ile Pro Gly Ile Pro Thr Val Leu Asn
156             390             395             400
158 ccc gtc cag gtc agc tcc ggc cct tct gag tcc tca cag aac aag ccc   1305
159 Pro Val Gln Val Ser Ser Gly Pro Ser Glu Ser Ser Gln Asn Lys Pro
160             405             410             415
162 acg agt gag tct gca gtg agc agc act ggt gac ccg atg cac aac aag   1353
163 Thr Ser Glu Ser Ala Val Ser Ser Thr Gly Asp Pro Met His Asn Lys
164         420             425             430
166 agg tcc aag atc aaa ccc gat gaa gac ctc ccc agc cca ggg gct cgg   1401
167 Arg Ser Lys Ile Lys Pro Asp Glu Asp Leu Pro Ser Pro Gly Ala Arg
168     435             440             445
170 ggg cag cag gaa cag ccc gaa gga aca acc ctt gtc aag gag gaa ggg   1449
171 Gly Gln Gln Glu Gln Pro Glu Gly Thr Thr Leu Val Lys Glu Glu Gly
172 450             455             460             465
174 gac aaa gat gaa agc aaa cag gag cct gaa gtc atc tat gag aca aac   1497
175 Asp Lys Asp Glu Ser Lys Gln Glu Pro Glu Val Ile Tyr Glu Thr Asn
176             470             475             480
178 tgc cac tgg gaa ggc tgc gcg agg gag ttc gac acc caa gag cag ctt   1545
179 Cys His Trp Glu Gly Cys Ala Arg Glu Phe Asp Thr Gln Glu Gln Leu
180             485             490             495
182 gtg cac cat ata aat aac gac cat att cat gga gag aag aag gag ttc   1593
183 Val His His Ile Asn Asn Asp His Ile His Gly Glu Lys Lys Glu Phe
184         500             505             510
186 gtg tgc agg tgg ctg gac tgc tca aga gag cag aaa ccc ttc aaa gcc   1641
187 Val Cys Arg Trp Leu Asp Cys Ser Arg Glu Gln Lys Pro Phe Lys Ala
188     515             520             525
190 cag tat atg ttg gta gtg cat atg aga aga cac acg ggc gag aag cct   1689
191 Gln Tyr Met Leu Val Val His Met Arg Arg His Thr Gly Glu Lys Pro
192 530             535             540             545
194 cac aaa tgc act ttt gaa ggt tgc aca aag gcc tac tcg aga cta gaa   1737
195 His Lys Cys Thr Phe Glu Gly Cys Thr Lys Ala Tyr Ser Arg Leu Glu
196                 550             555             560
198 aac ttg aaa aca cac ttg aga tct cac act gga gag aaa cca tac gtc   1785
199 Asn Leu Lys Thr His Leu Arg Ser His Thr Gly Glu Lys Pro Tyr Val
200             565             570             575
202 tgt gag cac gaa ggt tgc aac aag gct ttc tca aat gcc tct gat cgc   1833
203 Cys Glu His Glu Gly Cys Asn Lys Ala Phe Ser Asn Ala Ser Asp Arg
```

```
204        580                    585                590
206 gcc aaa cac caa aac aga acg cat tcc aat gag aaa cca tat gtg tgc    1881
207 Ala Lys His Gln Asn Arg Thr His Ser Asn Glu Lys Pro Tyr Val Cys
208        595                    600                605
210 aaa atc cca ggc tgc act aag cgt tac aca gac cca agc tcc ctc cgg    1929
211 Lys Ile Pro Gly Cys Thr Lys Arg Tyr Thr Asp Pro Ser Ser Leu Arg
212 610                          615                620                625
214 aaa cat gtg aag aca gtg cat ggc cca gag gct cat gtc acc aag aag    1977
215 Lys His Val Lys Thr Val His Gly Pro Glu Ala His Val Thr Lys Lys
216        630                                635                640
218 cag cga ggg gac atc cat cct cgg ccg cca ccc ccg aga gat tcc ggc    2025
219 Gln Arg Gly Asp Ile His Pro Arg Pro Pro Pro Pro Arg Asp Ser Gly
220        645                    650                       655
222 agc cat tca cag tcc agg tcg cct ggc cga ccg act cag gga gcc ctt    2073
223 Ser His Ser Gln Ser Arg Ser Pro Gly Arg Pro Thr Gln Gly Ala Leu
224        660                    665                670
226 ggt gag cag cag gac ctc agc aac act acc tca aag cgg gaa gaa tgc    2121
227 Gly Glu Gln Gln Asp Leu Ser Asn Thr Thr Ser Lys Arg Glu Glu Cys
228        675                    680                685
230 ctc cag gtg aaa acc gtc aag gca gag aag cca atg aca tct cag cca    2169
231 Leu Gln Val Lys Thr Val Lys Ala Glu Lys Pro Met Thr Ser Gln Pro
232 690                          695                700                705
234 agc cct ggt ggt cag tct tca tgc agc agc caa cag tcc ccc atc agc    2217
235 Ser Pro Gly Gly Gln Ser Ser Cys Ser Ser Gln Gln Ser Pro Ile Ser
236        710                    715                720
238 aac tat tcc aac agt ggg ctc gag ctt cct ctg acc gat gga ggt agt    2265
239 Asn Tyr Ser Asn Ser Gly Leu Glu Leu Pro Leu Thr Asp Gly Gly Ser
240        725                    730                       735
242 ata gga gac ctc agt gcc atc gat gaa acc cca atc atg gac tca acc    2313
243 Ile Gly Asp Leu Ser Ala Ile Asp Glu Thr Pro Ile Met Asp Ser Thr
244        740                    745                750
246 att tcc act gca acc aca gcc ctt gct ttg caa gcc agg aga aac ccg    2361
247 Ile Ser Thr Ala Thr Thr Ala Leu Ala Leu Gln Ala Arg Arg Asn Pro
248        755                    760                765
250 gca ggg acc aaa tgg atg gag cac gta aaa cta gaa agg cta aaa caa    2409
251 Ala Gly Thr Lys Trp Met Glu His Val Lys Leu Glu Arg Leu Lys Gln
252 770                          775                780                785
254 gtg aat gga atg ttt ccg cga ctg aac ccc att cta ccc cct aaa gcc    2457
255 Val Asn Gly Met Phe Pro Arg Leu Asn Pro Ile Leu Pro Pro Lys Ala
256        790                    795                800
258 cct gcg gtc tct cct ctc ata gga aat ggc aca cag tcc aac aac acc    2505
259 Pro Ala Val Ser Pro Leu Ile Gly Asn Gly Thr Gln Ser Asn Asn Thr
260        805                    810                815
262 tgc agc ttg ggt ggg ccc atg acg ctt ctc ccg ggc aga agc gac ctc    2553
263 Cys Ser Leu Gly Gly Pro Met Thr Leu Leu Pro Gly Arg Ser Asp Leu
264        820                    825                830
266 tct ggg gtg gac gtc act atg ctg aac atg ctc aac aga agg gac agc    2601
267 Ser Gly Val Asp Val Thr Met Leu Asn Met Leu Asn Arg Arg Asp Ser
268        835                    840                845
```

```
270 agc gcc agc acc atc agc tcg gcc tac ctg agc agc cgc cgc tcc tca        2649
271 Ser Ala Ser Thr Ile Ser Ser Ala Tyr Leu Ser Ser Arg Arg Ser Ser
272 850                        855                860            865
274 ggg atc tcg ccc tgc ttc tcc agc cgc cgc tcc agc gag gcg tca cag        2697
275 Gly Ile Ser Pro Cys Phe Ser Ser Arg Arg Ser Ser Glu Ala Ser Gln
276                         870                875              880
278 gcc gag ggc cgg ccg cag aac gtg agc gtg gcc gac tcc tac gac ccc        2745
279 Ala Glu Gly Arg Pro Gln Asn Val Ser Val Ala Asp Ser Tyr Asp Pro
280         885                      890                895
282 atc tcc acc gac gcc tcg cgc cgc tcc agc gaa gcc agc cag agc gac        2793
283 Ile Ser Thr Asp Ala Ser Arg Arg Ser Ser Glu Ala Ser Gln Ser Asp
284         900                      905                910
286 ggc ctg ccc agc ctg ctc agc ctc acg ccc gcc cag cag tac cgc ctc        2841
287 Gly Leu Pro Ser Leu Leu Ser Leu Thr Pro Ala Gln Gln Tyr Arg Leu
288     915                      920                925
290 aag gcc aag tac gcg gct gcc aca gga ggg ccg ccg ccg acg .ccc ctg       2889
291 Lys Ala Lys Tyr Ala Ala Ala Thr Gly Gly Pro Pro Pro Thr Pro Leu
292 930                      935                940              945
294 ccc aac atg gag agg atg agc ctg aag acg cgc ctg gcg ctg ctc ggg        2937
295 Pro Asn Met Glu Arg Met Ser Leu Lys Thr Arg Leu Ala Leu Leu Gly
296                         950                955              960
298 gat gcc ctc gag cct ggc gtg gcc ctg cct cca gtt cat gcc ccg agg        2985
299 Asp Ala Leu Glu Pro Gly Val Ala Leu Pro Pro Val His Ala Pro Arg
300             965                      970                975
302 agg tgc agc gac ggg gga gcc cac ggc tac ggg cgg cgc cac ctg cag        3033
303 Arg Cys Ser Asp Gly Gly Ala His Gly Tyr Gly Arg Arg His Leu Gln
304 ·           980                      985            990
306 ccg cac gat gcg ctg ggc cac ggc gtg agg agg gcc agc gac ccg gtg        3081
307 Pro His Asp Ala Leu Gly His Gly Val Arg Arg Ala Ser Asp Pro Val
308     ·995                      1000                1005
310 cgg aca ggc tcc gag ggc ctg gcc ctg cct cgt gtg ccg cgc ttc agc        3129
311 Arg Thr Gly Ser Glu Gly Leu Ala Leu Pro Arg Val Pro Arg Phe Ser
312 1010                    1015               1020               1025
314 agc ctc agc agc tgc aac ccc ccg gcg atg gcc acg tcc gcg gag aag        3177
315 Ser Leu Ser Ser Cys Asn Pro Pro Ala Met Ala Thr Ser Ala Glu Lys
316                         1030               1035               1040
318 cgc agt ctc gtg ctt cag aat tac acg cgg ccc gag ggc ggc cag tcc        3225
319 Arg Ser Leu Val Leu Gln Asn Tyr Thr Arg Pro Glu Gly Gly Gln Ser
320             1045                 1050               1055
322 cga aac ttc cac tcg tcc ccc tgt cct ccc agc atc acc gag aac gtc        3273
323 Arg Asn Phe His Ser Ser Pro Cys Pro Pro Ser Ile Thr Glu Asn Val
324         1060                     1065               1070
326 acc ctg gag tcc ctg acc atg gac gct gat gcc aac ctg aac gat gag        3321
327 Thr Leu Glu Ser Leu Thr Met Asp Ala Asp Ala Asn Leu Asn Asp Glu
328     1075                    1080               1085
330 gat ttc ctg ccg gac gac gtg gtg cag tat tta aat tcc cag aac caa        3369
331 Asp Phe Leu Pro Asp Asp Val Val Gln Tyr Leu Asn Ser Gln Asn Gln
332 1090                    1095               1100               1105
334 gca ggg tac gag cag cac ttc ccc agc gcc ctc ccg gac gac agc aaa        3417
```

VERIFICATION SUMMARY
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DATE: 08/02/2001
TIME: 10:56:09

Input Set : **A:\RTS-0258 Sequence Listing.txt**
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date